

SEQUENCE LISTING

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Zenke, Gerhard

<120> TITLE: ATOMIC STRUCTURE OF THE CATALYTIC DOMAIN
FOR USE IN DESIGNING AND IDENTIFYING INHIBITORS OF ZAP-70
KINASE

<130> DOCKET/FILE REFERENCE: 4-32688A

<140> CURRENT APPLICATION NUMBER: US10/528,709
<141> FILING DATE: 2003-09-25

<150> PRIOR APPLICATION NUMBER: PCT/EP03/10686
<151> FILING DATE: 2003-09-25

<150> PRIOR APPLICATION NUMBER: 60/413,704
<151> FILING DATE: 2002-09-26

<160> NUMBER OF SEQUENCES: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO:1
<211> LENGTH: 619
<212> TYPE: PRT
<213> ORGANISM:Homo sapiens

<400> SEQ ID NO:1
Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15
Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30
Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45
Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60
Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80
Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95
Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110
Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys

	165	170	175												
Leu	Tyr	Ser	Gly	Ala	Gln	Thr	Asp	Gly	Lys	Phe	Leu	Leu	Arg	Pro	Arg
															190
180								185							
Lys	Glu	Gln	Gly	Thr	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Gly	Lys	Thr	Val
															205
195								200							
Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro
															220
210							215								
Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys
															240
225				230						235					
Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn
									250						255
245															
Ser	Ser	Ala	Ser	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala
															270
260							265								
His	Pro	Ser	Thr	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn
											280				285
275															
Ser	Asp	Gly	Tyr	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys
											300				
290							295								
Pro	Arg	Pro	Met	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser
										310		315			320
305															
Asp	Pro	Glu	Glu	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn
										325		330			335
Leu	Leu	Ile	Ala	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val
									340		345				350
Arg	Gln	Gly	Val	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile
									355		360				365
Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met	Met
									370		375				380
Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val	Arg
									385		390				400
Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu	Met
									405		410				415
Ala	Gly	Gly	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu	Glu	
									420		425				430
Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly
									435		440				445
Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala
									450		455				460
Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp	Phe
									465		470				480
Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg
									485		490				495
Ser	Ala	Gly	Lys	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn
									500		505				510
Phe	Arg	Lys	Phe	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr
									515		520				525
Met	Trp	Glu	Ala	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met	Lys
									530		535				540
Gly	Pro	Glu	Val	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu	Cys
									545		550				560
Pro	Pro	Glu	Cys	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys	Trp
									565		570				575
Ile	Tyr	Lys	Trp	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln	Arg
									580		585				590
Met	Arg	Ala	Cys	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro	Pro
									595		600				605
Gly	Ser	Thr	Gln	Lys	Ala	Glu	Ala	Ala	Cys	Ala					
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<210> SEQ ID NO:2
<211> LENGTH: 322
<212> TYPE: PRT
<213> ORGANISM:Homo sapiens

<400> SEQ ID NO:2
Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met Asp Thr Ser
1 5 10 15
Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys
20 25 30
Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly
35 40 45
Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys
50 55 60
Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys
65 70 75 80
Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu
85 90 95
Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala
100 105 110
Leu Met Leu Val Met Glu Met Ala Gly Gly Pro Leu His Lys Phe
115 120 125
Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu
130 135 140
Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe
145 150 155 160
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His
165 170 175
Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp
180 185 190
Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp
195 200 205
Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp
210 215 220
Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln
225 230 235 240
Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu
245 250 255
Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr
260 265 270
Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp
275 280 285
Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala
290 295 300
Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala
305 310 315 320
Cys Ala

<210> SEQ ID NO:3
<211> LENGTH: 74
<212> TYPE: DNA
<213> ORGANISM:Unknown

<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide MG474

<400> SEQ ID NO:3
cagatggata caccctgag ccagcactgg aagttctgtt ccaggggccc cgcataacgt 60
ccccagacaa accg 74

<210> SEQ ID NO:4
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM:Unknown

<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide RS366

<400> SEQ ID NO:4
acaacgcaca gaatcttagcg 20

<210> SEQ ID NO:5
<211> LENGTH: 74
<212> TYPE: DNA
<213> ORGANISM:Unknown

<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide MG475

<400> SEQ ID NO:5
cacactccca gcccacccat ccacgctgga agttctgttc caggggcccct tgactcatcc 60
tcagagacga atcg 74

<210> SEQ ID NO:6
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM:Unknown

<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide MG479

<400> SEQ ID NO:6
gctcgaattc tcaatgtatga tgatgtatgtat gggcacaggc agcctcagcc ttctgtg 57